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0|0|0 Intelligenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file AA436049VS09646624-2.res made by spaul on Fri 9 Apr 104 11:38:08-PDT.

Query sequence being compared: aa436049 (1-449)
Number of sequences searched: 2
Number of scores above cutoff: 2

Results of the initial comparison of aa436049 (1-449) with:
File: US09646624C.pep

```

100-
N -
U -
M -
B -
E -
R -
O -
F -
S -
E -
U -
N -
C -
E -
S -
SCORE 0 6 11 17 23 28 34 40 45 51
SIDEV -8 -6 -1

```

PARAMETERS

Similarity matrix PAM-150 K-cuple 1
Threshold level of sim. 16%
Translation Frame 6
Mismatch penalty 5.00 Joining penalty 20
Gap penalty 0.33 Window size 449
Gap size penalty 1
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
50 51 0.71
Times: CPU Total Elapsed
00:00:00.00 00:00:00.00
Number of residues: 563
Number of sequences searched: 2
Number of scores above cutoff: 2

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sign.	Frame
1. US-09-646-624C-2	Sequence 2, Application U	282	51	52	1.41	1
2. US-09-646-624C-4	Sequence 4, Application U	281	50	51	0.00	1

1. aa436049 (1-449)
US-09-646-624C-2 Sequence 2, Application US/09646624C
Initial Score = 51 Optimized Score = 52 Significance = 1.41
Residue Identity = 90% Matches = 50 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0
Translation Frame = 1

```

X 10 20
INHDGDSGGPIVNCNOSTLQGIT
GWGSTSPQLRLPHLRCANITIEHOKCENAYPGNITDTWVCASVQEGKDCGDSGGPIVNCNOSTLQGIT
180 190 200 210 220 230 240
SMGQDPFCATIRKRGVYTKYCKYVDWIOETMKNKXGPTTHSPSPSISTWCLVPYASVKKPKAKTLVHSLG
250 260 270 280 X
LIDYRRCCHI

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